

&lt;!--StartFragment--&gt;RESULT 1

HAL2\_YEAST

ID HAL2\_YEAST STANDARD; PRT; 357 AA.

AC P32179;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) (3'(2'),5-

DE bisphosphonucleoside 3'(2')-phosphohydrolase) (DPNPase) (Halotolerance protein HAL2).

GN Name=HAL2; Synonyms=MET22; OrderedLocusNames=YOL064C;

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI\_TaxID=4932;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=93345455; PubMed=8393782;

RA Glaeser H.-U., Thomas D., Gaxiola R., Montrichard F.,

RA Surdin-Kerjan Y., Serrano R.;

RT "Salt tolerance and methionine biosynthesis in Saccharomyces

RT cerevisiae involve a putative phosphatase gene.";

RL EMBO J. 12:3105-3110(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=97321807; PubMed=9178509;

RX DOI=10.1002/(SICI)1097-0061(199705)13:6&lt;583::AID-YEA111&gt;3.0.CO;2-Y;

RA Tzermia M., Katsoulou C., Alexandraki D.;

RT "Sequence analysis of a 33.2 kb segment from the left arm of yeast

RT chromosome XV reveals eight known genes and ten new open reading

RT frames including homologues of ABC transporters, inositol phosphatases

RT and human expressed sequence tags.";

RL Yeast 13:583-589(1997).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=S288c / FY1679;

RX MEDLINE=97313270; PubMed=9169874;

RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansorge W.,

RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,

RA Boyer J., Camasses A., Casamayor A., Casas C., Cheret G.,

RA Cziepluch C., Daignan-Fornier B., Dang D.V., de Haan M., Delius H.,

RA Durand P., Fairhead C., Feldmann H., Gaillon L., Galisson F.,

RA Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,

RA Habbig B., Hand N.J., Hani J., Hattenhorst U., Hebling U.,

RA Hernando Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,

RA Hollenberg C.P., Hughes B., Jauniaux J.-C., Kalogeropoulos A.,

RA Katsoulou C., Kordes E., Lafuente M.J., Landt O., Louis E.J.,

RA Maarse A.C., Madania A., Mannhaupt G., Marck C., Martin R.P.,

RA Mewes H.-W., Michaux G., Paces V., Parle-McDermott A.G., Pearson B.M.,

RA Perrin A., Pettersson B., Poch O., Pohl T.M., Poiray R.,

RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rechmann S.,

RA Schwager C., Schweizer M., Sor F., Sterky F., Tarassov I.A.,

RA Teodoru C., Tettelin H., Thierry A., Tobiasch E., Tzermia M.,

RA Uhlen M., Unseld M., Valens M., Vandenbol M., Vetter I., Vlcek C.,

RA Voet M., Volckaert G., Voss H., Wambutt R., Wedler H., Wiemann S.,

RA Winsor B., Wolfe K.H., Zollner A., Zumstein E., Kleine K.;

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";

RL Nature 387:98-102(1997).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) IN COMPLEX WITH MAGNESIUM IONS

RP AND AMP.

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RX  MEDLINE=20123982; PubMed=10656801; DOI=10.1006/jmbi.1999.3408;
RA  Albert A., Yenush L., Gil-Mascarell M.R., Rodriguez P.L., Patel S.,
RA  Martinez-Ripoll M., Blundell T.L., Serrano R.;
RT  "X-ray structure of yeast Hal2p, a major target of lithium and sodium
RT  toxicity, and identification of framework interactions determining
RT  cation sensitivity.";
RL  J. Mol. Biol. 295:927-938(2000).
CC  -!- FUNCTION: Converts adenosine 3'-phosphate 5'-phosphosulfate (PAPS)
CC      to adenosine 5'-phosphosulfate (APS) and 3'(2')-phosphoadenosine
CC      5'- phosphate (PAP) to AMP. Regulates the flux of sulfur in the
CC      sulfur-activation pathway by converting PAPS to APS. Involved in
CC      salt tolerance. Confers resistance to lithium.
CC  -!- CATALYTIC ACTIVITY: Adenosine 3',5'-bisphosphate + H(2)O =
CC      adenosine 5'-phosphate + phosphate.
CC  -!- COFACTOR: Magnesium.
CC  -!- INDUCTION: By salt stress.
CC  -!- SIMILARITY: Belongs to the inositol monophosphatase family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; X72847; CAA51361.1; -; Genomic_DNA.
DR  EMBL; Z74806; CAA99074.1; -; Genomic_DNA.
DR  PIR; S35318; S35318.
DR  PDB; 1K9Y; X-ray; A=1-357.
DR  PDB; 1K9Z; X-ray; A=1-357.
DR  PDB; 1KA0; X-ray; A=1-357.
DR  PDB; 1KA1; X-ray; A=1-357.
DR  PDB; 1QGX; X-ray; A=1-357.
DR  GermOnline; 143487; -.
DR  Ensembl; YOL064C; Saccharomyces cerevisiae.
DR  SGD; S000005425; MET22.
DR  GO; GO:0005737; C:cytoplasm; IDA.
DR  GO; GO:0008441; F:3'(2'),5'-bisphosphate nucleotidase activity; TAS.
DR  GO; GO:0042538; P:hyperosmotic salinity response; TAS.
DR  GO; GO:0009086; P:methionine biosynthesis; TAS.
DR  GO; GO:0000103; P:sulfate assimilation; TAS.
DR  InterPro; IPR006239; Bisphos_HAL2.
DR  InterPro; IPR000760; Inositol_P.
DR  Pfam; PF00459; Inositol_P; 1.
DR  PRINTS; PR00378; INOSPHPTASE.
DR  ProDom; PD023420; Inositol_P; 1.
DR  TIGRFAMs; TIGR01330; bisphos_HAL2; 1.
DR  PROSITE; PS00629; IMP_1; 1.
DR  PROSITE; PS00630; IMP_2; 1.
KW  3D-structure; Complete proteome; Hydrolase; Lithium; Magnesium;
KW  Metal-binding.
FT  METAL          72      72      Magnesium 2.
FT  METAL          142     142     Magnesium 1 and 2.
FT  METAL          145     145     Magnesium 1.
FT  METAL          294     294     Magnesium 1.
FT  HELIX           4      30
FT  TURN            31      34
FT  STRAND          36      38
FT  TURN            40      41
FT  STRAND          44      46
FT  HELIX           47      63
FT  TURN            65      66

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FT	STRAND	69	71
FT	TURN	76	77
FT	HELIX	80	100
FT	TURN	104	105
FT	HELIX	118	126
FT	TURN	127	128
FT	STRAND	129	129
FT	STRAND	137	145
FT	TURN	146	146
FT	HELIX	147	151
FT	TURN	152	153
FT	STRAND	157	164
FT	TURN	165	166
FT	STRAND	167	175
FT	TURN	176	177
FT	HELIX	180	183
FT	TURN	184	184
FT	TURN	189	190
FT	HELIX	191	194
FT	STRAND	196	201
FT	TURN	202	203
FT	STRAND	206	210
FT	TURN	211	213
FT	STRAND	218	219
FT	HELIX	228	230
FT	STRAND	232	235
FT	TURN	239	241
FT	HELIX	244	253
FT	TURN	254	255
FT	STRAND	258	261
FT	TURN	265	265
FT	HELIX	266	273
FT	TURN	274	274
FT	STRAND	278	281
FT	TURN	286	287
FT	STRAND	291	291
FT	HELIX	292	294
FT	TURN	295	295
FT	HELIX	296	304
FT	TURN	305	306
FT	STRAND	308	310
FT	STRAND	317	317
FT	TURN	320	321
FT	STRAND	325	325
FT	STRAND	331	334
FT	HELIX	338	353
FT	TURN	354	354
SQ	SEQUENCE	357 AA;	39149 MW; AB2E5F90B285702B CRC64;

Query Match 100.0%; Score 1838; DB 1; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-141;  
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIAK	60
Db	2	ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIAK	61
Qy	61	SNFPDDKVVGESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV	120
Db	62	SNFPDDKVVGESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV	121

Qy	121	RQIIDFGNYEGGRKGREFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS	180
Db	122	RQIIDFGNYEGGRKGREFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS	181
Qy	181	SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH	240
Db	182	SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH	241
Qy	241	SSHDEQTAIKNKLNISKSLHLD SQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVI	300
Db	242	SSHDEQTAIKNKLNISKSLHLD SQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVI	301
Qy	301	VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA	356
Db	302	VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA	357

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<!--EndFragment-->
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